

Sloboodjaisky



1600

RAW SEQUENCE LISTING

DATE: 01/29/2003

PATENT APPLICATION: US/09/712,768A

TIME: 19:32:41

#12

Input Set : N:\Crf4\Refhold\I712768A.raw

Output Set: N:\CRF4\01292003\I712768A.raw

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1 <110> APPLICANT: Asakura, Akira
 2 Hoshino, Tatsuo
 3 Shinjoh, Masako
 4 <120> TITLE OF INVENTION: Cytochrome C Oxidase Enzyme Complex
 5 <130> FILE REFERENCE: C38435/111693
 C--> 6 <140> CURRENT APPLICATION NUMBER: US/09/712,768A
 7 <141> CURRENT FILING DATE: 2002-11-13
 8 <150> PRIOR APPLICATION NUMBER: EP 99122842
 9 <151> PRIOR FILING DATE: 1999-11-17
 10 <160> NUMBER OF SEQ ID NOS: 36
 11 <170> SOFTWARE: PatentIn version 3.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1674
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Gluconobacter oxydans
 17 <220> FEATURE:
 18 <221> NAME/KEY: CDS
 19 <222> LOCATION: (1)..(1674)
 20 <223> OTHER INFORMATION:
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 24 1 5 10 15
 25 ttc ttc acg cgc tgg ttc atg tcg acc aac cac aaa gac atc ggt ctg 96
 26 Phe Phe Thr Arg Trp Phe Met Ser Thr Asn His Lys Asp Ile Gly Leu
 27 20 25 30
 28 cta tac ctt gta gcg gct ggt gtt gtt ggt ttc att tcc gtc ctg ttc 144
 29 Leu Tyr Leu Val Ala Ala Gly Val Val Gly Phe Ile Ser Val Leu Phe
 30 35 40 45
 31 acc gtc tac atg cgc ctt gag ctg atg gat ccg ggt gtt cag tac atg 192
 32 Thr Val Tyr Met Arg Leu Glu Leu Met Asp Pro Gly Val Gln Tyr Met
 33 50 55 60
 34 tgc ctt gaa ggc gca cgt ctg atc gcg gat gcc tcg cag aca tgt acg 240
 35 Cys Leu Glu Gly Ala Arg Leu Ile Ala Asp Ala Ser Gln Thr Cys Thr
 36 65 70 75 80
 37 gcg aac gga cac ctg tgg aac gtc atg gtt acc tac cat ggt att ctg 288
 38 Ala Asn Gly His Leu Trp Asn Val Met Val Thr Tyr His Gly Ile Leu
 39 85 90 95
 40 atg atg ttc ttt gtg ggt atc ccc gca ttg ttc ggt ggt ttt ggt aac 336
 41 Met Met Phe Phe Val Gly Ile Pro Ala Leu Phe Gly Gly Phe Gly Asn
 42 100 105 110
 43 tat ctg atg ccg ctg caa atc ggc gct ccg gat atg gcc ttc ccg cgt 384
 44 Tyr Leu Met Pro Leu Gln Ile Gly Ala Pro Asp Met Ala Phe Pro Arg

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45			115					120				125					
46	atg	aac	aac	ctg	tcg	ttc	tgg	ctg	ttc	att	gcc	ggt	acc	gcg	atg	ggc	432
47	Met	Asn	Asn	Leu	Ser	Phe	Trp	Leu	Phe	Ile	Ala	Gly	Thr	Ala	Met	Gly	
48		130					135					140					
49	gtg	gct	tcg	ctg	ttc	gca	ccg	ggc	ggt	gac	ggt	cag	ctg	ggt	tcg	ggc	480
50	Val	Ala	Ser	Leu	Phe	Ala	Pro	Gly	Gly	Asp	Gly	Gln	Leu	Gly	Ser	Gly	
51	145					150					155					160	
52	gtt	ggt	tgg	gtt	ctg	tac	ccg	ccg	ctg	tcg	acc	cgc	gaa	gct	ggc	tat	528
53	Val	Gly	Trp	Val	Leu	Tyr	Pro	Pro	Leu	Ser	Thr	Arg	Glu	Ala	Gly	Tyr	
54					165					170					175		
55	tcg	atg	gac	ctc	gcg	att	ttc	gcg	gtt	cac	ttg	tcg	ggt	gcc	tcc	tcg	576
56	Ser	Met	Asp	Leu	Ala	Ile	Phe	Ala	Val	His	Leu	Ser	Gly	Ala	Ser	Ser	
57			180					185					190				
58	atc	atg	ggc	gcg	atc	aac	atg	atc	acg	acc	ttc	ttg	aac	atg	cgc	gcc	624
59	Ile	Met	Gly	Ala	Ile	Asn	Met	Ile	Thr	Thr	Phe	Leu	Asn	Met	Arg	Ala	
60			195					200					205				
61	ccc	ggc	atg	acg	ctg	cac	aaa	gtg	ccg	ttg	ttc	tcg	tgg	tcg	atc	ttt	672
62	Pro	Gly	Met	Thr	Leu	His	Lys	Val	Pro	Leu	Phe	Ser	Trp	Ser	Ile	Phe	
63		210				215						220					
64	atc	acg	gct	tgg	ctg	atc	ctg	ctg	gcg	ctg	ccg	gtt	ctg	gct	ggt	gca	720
65	Ile	Thr	Ala	Trp	Leu	Ile	Leu	Leu	Ala	Leu	Pro	Val	Leu	Ala	Gly	Ala	
66	225					230					235					240	
67	atc	acc	atg	ctg	ctg	acc	gac	cgt	aac	ttc	ggc	acg	acc	ttc	ttc	aat	768
68	Ile	Thr	Met	Leu	Leu	Thr	Asp	Arg	Asn	Phe	Gly	Thr	Thr	Phe	Phe	Asn	
69					245					250					255		
70	cct	gct	ggc	ggc	ggt	gac	ccg	att	ctg	tac	caa	cac	atc	ctg	tgg	ttc	816
71	Pro	Ala	Gly	Gly	Gly	Asp	Pro	Ile	Leu	Tyr	Gln	His	Ile	Leu	Trp	Phe	
72			260					265					270				
73	ttt	ggg	cac	ccg	gaa	gtg	tac	atc	atc	att	ctg	ccc	ggc	ttt	ggc	atc	864
74	Phe	Gly	His	Pro	Glu	Val	Tyr	Ile	Ile	Ile	Leu	Pro	Gly	Phe	Gly	Ile	
75			275					280					285				
76	atc	agc	cat	gtc	gtg	tcg	acc	ttc	tcg	aaa	aag	ccg	gtc	ttc	ggt	tac	912
77	Ile	Ser	His	Val	Val	Ser	Thr	Phe	Ser	Lys	Lys	Pro	Val	Phe	Gly	Tyr	
78		290					295					300					
79	ctg	ccg	atg	gtc	tat	gca	atg	gtg	gca	atc	ggt	gtt	ctg	ggc	ttt	gtc	960
80	Leu	Pro	Met	Val	Tyr	Ala	Met	Val	Ala	Ile	Gly	Val	Leu	Gly	Phe	Val	
81	305					310					315						

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95      Gly Gly Val Thr Gly Ile Val Leu Ala Gln Ala Gly Leu Asp Arg Ala
96      385                      390                      395                      400
97      tat cac gac acc tat tac gtg gtg gcg cac ttc cat tat gtg atg tcg      1248
98      Tyr His Asp Thr Tyr Tyr Val Val Ala His Phe His Tyr Val Met Ser
99                      405                      410                      415
100     ctg ggt gcg atc ttt gcg atc ttc gcc ggt atc tac ttt tac atg ccg      1296
101     Leu Gly Ala Ile Phe Ala Ile Phe Ala Gly Ile Tyr Phe Tyr Met Pro
102                      420                      425                      430
103     aag ttc tcg ggc cgc gct ttc ccg gaa tgg gct gca aag ctg cac ttc      1344
104     Lys Phe Ser Gly Arg Ala Phe Pro Glu Trp Ala Ala Lys Leu His Phe
105                      435                      440                      445
106     tgg acc ttc ttc atc ggt gcg aac gtc acg ttc ttc ccg cag cac ttc      1392
107     Trp Thr Phe Phe Ile Gly Ala Asn Val Thr Phe Phe Pro Gln His Phe
108                      450                      455                      460
109     ctg gga cgt cag ggt atg ccg cgc cgt tac atc gac tat ccc gaa gcc      1440
110     Leu Gly Arg Gln Gly Met Pro Arg Arg Tyr Ile Asp Tyr Pro Glu Ala
111     465                      470                      475                      480
112     ttc gcg ctg tgg aac aaa gtc tcg tcc tat ggt gcg ttc ctg gcc ttc      1488
113     Phe Ala Leu Trp Asn Lys Val Ser Ser Tyr Gly Ala Phe Leu Ala Phe
114                      485                      490                      495
115     gcc tcg ttc ctg ttc ttc atc gtg atc ttt gtc tat acg ctg gtt gct      1536
116     Ala Ser Phe Leu Phe Phe Ile Val Ile Phe Val Tyr Thr Leu Val Ala
117                      500                      505                      510
118     ggc cgc cgc gag acc cgt ccg aac ccg tgg ggc gaa ttc gcc gat acg      1584
119     Gly Arg Arg Glu Thr Arg Pro Asn Pro Trp Gly Glu Phe Ala Asp Thr
120                      515                      520                      525
121     ctg gaa tgg acg ctg cca tca ccg cct ccg gcc cac acg ttc gaa acg      1632
122     Leu Glu Trp Thr Leu Pro Ser Pro Pro Pro Ala His Thr Phe Glu Thr
123                      530                      535                      540
124     ctg ccc aag cgc tcg gac tgg gac aag cat ccc tcg cac taa      1674
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128 <210> SEQ ID NO: 2
129 <211> LENGTH: 557
130 <212> TYPE: PRT
131 <213> ORGANISM: Gluconobacter oxydans
132 <400> SEQUENCE: 2
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137     Leu Tyr Leu Val Ala Ala Gly Val Val Gly Phe Ile Ser Val Leu Phe
138     35                      40                      45
139     Thr Val Tyr Met Arg Leu Glu Leu Met Asp Pro Gly Val Gln Tyr Met
140     50                      55                      60
141     Cys Leu Glu Gly Ala Arg Leu Ile Ala Asp Ala Ser Gln Thr Cys Thr
142     65                      70                      75                      80
143     Ala Asn Gly His Leu Trp Asn Val Met Val Thr Tyr His Gly Ile Leu

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Input Set : N:\Crf4\Refhold\I712768A.raw

Output Set: N:\CRF4\01292003\I712768A.raw

144				85				90				95
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146				100					105			110
147	Tyr	Leu	Met	Pro	Leu	Gln	Ile	Gly	Ala	Pro	Asp	Met
148				115					120			125
149	Met	Asn	Asn	Leu	Ser	Phe	Trp	Leu	Phe	Ile	Ala	Gly
150				130					135			140
151	Val	Ala	Ser	Leu	Phe	Ala	Pro	Gly	Gly	Asp	Gly	Gln
152				145					150			155
153	Val	Gly	Trp	Val	Leu	Tyr	Pro	Pro	Leu	Ser	Thr	Arg
154									165			170
155	Ser	Met	Asp	Leu	Ala	Ile	Phe	Ala	Val	His	Leu	Ser
156				180					185			190
157	Ile	Met	Gly	Ala	Ile	Asn	Met	Ile	Thr	Thr	Phe	Leu
158				195					200			205
159	Pro	Gly	Met	Thr	Leu	His	Lys	Val	Pro	Leu	Phe	Ser
160				210					215			220
161	Ile	Thr	Ala	Trp	Leu	Ile	Leu	Leu	Ala	Leu	Pro	Val
162				225					230			235
163	Ile	Thr	Met	Leu	Leu	Thr	Asp	Arg	Asn	Phe	Gly	Thr
164									245			250
165	Pro	Ala	Gly	Gly	Gly	Asp	Pro	Ile	Leu	Tyr	Gln	His
166				260					265			270
167	Phe	Gly	His	Pro	Glu	Val	Tyr	Ile	Ile	Ile	Leu	Pro
168				275					280			285
169	Ile	Ser	His	Val	Val	Ser	Thr	Phe	Ser	Lys	Lys	Pro
170				290					295			300
171	Leu	Pro	Met	Val	Tyr	Ala	Met	Val	Ala	Ile	Gly	Val
172				305					310			315
173	Val	Trp	Ala	His	His	Met	Tyr	Thr	Val	Gly	Met	Ser
174									325			330
175	Ser	Tyr	Phe	Met	Leu	Ala	Thr	Met	Val	Ile	Ala	Val
176				340					345			350
177	Lys	Ile	Phe	Ser	Trp	Ile	Ala	Thr	Met	Trp	Gly	Gly
178				355					360			365
179	Lys	Ser	Pro	Met	Leu	Trp	Ala	Phe	Gly	Phe	Met	Phe
180				370					375			380
181	Gly	Gly	Val	Thr	Gly	Ile	Val	Leu	Ala	Gln	Ala	Gly
182									385			390
183	Tyr	His	Asp	Thr	Tyr	Tyr	Val	Val	Ala	His	Phe	His
184									405			410
185	Leu	Gly	Ala	Ile	Phe	Ala	Ile	Phe	Ala	Gly	Ile	Tyr
186				420					425			430
187	Lys	Phe	Ser	Gly	Arg	Ala	Phe	Pro	Glu	Trp	Ala	Ala
188				435					440			445
189	Trp	Thr	Phe	Phe	Ile	Gly	Ala	Asn	Val	Thr	Phe	Phe
190				450					455			460
191	Leu	Gly	Arg	Gln	Gly	Met	Pro	Arg	Arg	Tyr	Ile	Asp
192									465			470

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Input Set : N:\Crf4\Refhold\I712768A.raw

Output Set: N:\CRF4\01292003\I712768A.raw

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193      Phe Ala Leu Trp Asn Lys Val Ser Ser Tyr Gly Ala Phe Leu Ala Phe
194              485              490              495
195      Ala Ser Phe Leu Phe Phe Ile Val Ile Phe Val Tyr Thr Leu Val Ala
196              500              505              510
197      Gly Arg Arg Glu Thr Arg Pro Asn Pro Trp Gly Glu Phe Ala Asp Thr
198              515              520              525
199      Leu Glu Trp Thr Leu Pro Ser Pro Pro Pro Ala His Thr Phe Glu Thr
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202              545              550              555
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205 <211> LENGTH: 132
206 <212> TYPE: DNA
207 <213> ORGANISM: Gluconobacter oxydans
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210 <222> LOCATION: (1)..(132)
211 <223> OTHER INFORMATION:
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214      Pro Leu Glu Ile Val Trp Thr Ile Val Pro Val Val Ile Leu Val Phe
215      1              5              10              15
216      atc ggt gcg ttc tcg ctg ccg gtg ctg ttc aaa cag caa gag ttc ccc      96
217      Ile Gly Ala Phe Ser Leu Pro Val Leu Phe Lys Gln Gln Glu Phe Pro
218      20              25              30
219      gag ggt gac atc gtc atc aac gtc gag ggt cgt agc      132
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221      35              40
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224 <211> LENGTH: 44
225 <212> TYPE: PRT
226 <213> ORGANISM: Gluconobacter oxydans
227 <400> SEQUENCE: 4
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230      Ile Gly Ala Phe Ser Leu Pro Val Leu Phe Lys Gln Gln Glu Phe Pro
231      20              25              30
232      Glu Gly Asp Ile Val Ile Asn Val Glu Gly Arg Ser
233      35              40
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236 <211> LENGTH: 114
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242 <223> OTHER INFORMATION:
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/712,768A

DATE: 01/29/2003
TIME: 19:32:42

Input Set : N:\Crf4\Refhold\I712768A.raw
Output Set: N:\CRF4\01292003\I712768A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:32; N Pos. 3,9
Seq#:33; N Pos. 9
Seq#:34; N Pos. 12
Seq#:35; N Pos. 3,9
Seq#:36; N Pos. 18